

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: DAUGHERTY, BRUCE L.
DEMARTINO, JULIE A.
SICILIANO, SALVATORE J.
SPRINGER, MARTIN S.
- (ii) TITLE OF THE INVENTION: EOSINOPHIL EOTAXIN RECEPTOR
- (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Merck & Co., Inc.
 - (B) STREET: P.O. Box 2000, 126 E. Lincoln Ave.
 - (C) CITY: Rahway
 - (D) STATE: NJ
 - (E) COUNTRY: USA
 - (F) ZIP: 07065-0900
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: DOS
 - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 60/016,158
 - (B) FILING DATE: 26-APR-1996
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Eric Thies, J.
 - (B) REGISTRATION NUMBER: 35,382
 - (C) REFERENCE/DOCKET NUMBER: 19634Y
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 908-594-3904
 - (B) TELEFAX: 908-594-4720
 - (C) TELEX:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met 1	Thr	Thr	Ser	Leu 5	Asp	Thr	Val	Glu	Thr 10	Phe	Gly	Thr	Thr	Ser 15	Tyr
Tyr	Asp	Asp	Val 20	Gly	Leu	Leu	Cys	Glu 25	Lys	Ala	Asp	Thr	Arg 30	Ala	Leu
Met	Ala	Gln 35	Phe	Val	Pro	Pro	Leu 40	Tyr	Ser	Leu	Val	Phe 45	Thr	Val	Gly
Leu	Leu 50	Gly	Asn	Val	Val	Val 55	Val	Met	Ile	Leu	Ile 60	Lys	Tyr	Arg	Arg
Leu 65	Arg	Ile	Met	Thr	Asn 70	Ile	Tyr	Leu	Leu	Asn 75	Leu	Ala	Ile	Ser	Asp 80
Leu	Leu	Phe	Leu 85	Val	Thr	Leu	Pro	Phe	Trp 90	Ile	His	Tyr	Val	Arg 95	Gly
His	Asn	Trp	Val 100	Phe	Gly	His	Gly	Met 105	Cys	Lys	Leu	Leu	Ser 110	Gly	Phe
Tyr	His	Thr 115	Gly	Leu	Tyr	Ser	Glu 120	Ile	Phe	Phe	Ile	Ile 125	Leu	Leu	Thr
Ile	Asp 130	Arg	Tyr	Leu	Ala 135	Ile	Val	His	Ala	Val	Phe 140	Ala	Leu	Arg	Ala
Arg 145	Thr	Val	Thr	Phe	Gly 150	Val	Ile	Thr	Ser	Ile 155	Val	Thr	Trp	Gly	Leu 160
Ala	Val	Leu	Ala 165	Ala	Leu	Pro	Glu	Phe	Ile 170	Phe	Tyr	Glu	Thr	Glu 175	Glu
Leu	Phe	Glu 180	Glu	Thr	Leu	Cys	Ser 185	Ala	Leu	Tyr	Pro	Glu	Asp 190	Thr	Val
Tyr	Ser 195	Trp	Arg	His	Phe	His	Thr 200	Leu	Arg	Met	Thr	Ile 205	Phe	Cys	Leu
Val	Leu 210	Pro	Leu	Leu	Val	Met 215	Ala	Ile	Cys	Tyr	Thr 220	Gly	Ile	Ile	Lys
Thr 225	Leu	Leu	Arg	Cys	Pro 230	Ser	Lys	Lys	Lys	Tyr 235	Lys	Ala	Ile	Arg	Leu 240
Ile	Phe	Val	Ile 245	Met	Ala	Val	Phe	Phe	Ile 250	Phe	Trp	Thr	Pro	Tyr 255	Asn
Val	Ala	Ile 260	Leu	Leu	Ser	Ser	Tyr	Gln 265	Ser	Ile	Leu	Phe 270	Gly	Asn	Asp
Cys	Glu 275	Arg	Ser	Lys	His	Leu	Asp 280	Leu	Val	Met	Leu	Val 285	Thr	Glu	Val
Ile	Ala 290	Tyr	Ser	His	Cys	Cys 295	Met	Asn	Pro	Val	Ile 300	Tyr	Ala	Phe	Val
Gly 305	Glu	Arg	Phe	Arg	Lys 310	Tyr	Leu	Arg	His	Phe 315	Phe	His	Arg	His	Leu 320
Leu	Met	His	Leu 325	Gly	Arg	Tyr	Ile	Pro	Phe 330	Leu	Pro	Ser	Glu	Lys 335	Leu
Glu	Arg	Thr	Ser 340	Ser	Val	Ser	Pro	Ser 345	Thr	Ala	Glu	Pro	Glu	Leu	Ser

Ile Val Phe

355

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1065 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATGACAACCT CACTAGATAC AGTTGAGACC TTTGGTACCA CATCCTACTA TGATGACGTG
60
GGCCTGCTCT GTGAAAAAGC TGATACCAGA GCACTGATGG CCCAGTTTGT GCCCCCGCTG
120
TACTCCCTGG TGTTCACTGT GGGCCTCTTG GGCAATGTGG TGGTGGTGAT GATCCTCATA
180
AAATACAGGA GGCTCCGAAT TATGACCAAC ATCTACCTGC TCAACCTGGC CATTTCCGAC
240
CTGCTCTTCC TCGTCACCCT TCCATTCTGG ATCCACTATG TCAGGGGGCA TAACTGGGTT
300
TTTGGCCATG GCATGTGTAA GCTCCTCTCA GGGTTTTATC ACACAGGCTT GTACAGCGAG
360
ATCTTTTTCA TAATCCTGCT GACAATCGAC AGGTACCTGG CCATTGTCCA TGCTGTGTTT
420
GCCCTTCGAG CCCGGACTGT CACTTTTGGT GTCATCACCA GCATCGTCAC CTGGGGCCTG
480
GCAGTGCTAG CAGCTCTTCC TGAATTTATC TTCTATGAGA CTGAAGAGTT GTTTGAAGAG
540
ACTCTTTGCA GTGCTCTTTA CCCAGAGGAT ACAGTATATA GCTGGAGGCA TTTCCACACT
600
CTGAGAATGA CCATCTTCTG TCTCGTTCTC CCTCTGCTCG TTATGGCCAT CTGCTACACA
660
GGAATCATCA AAACGCTGCT GAGGTGCCCC AGTAAAAAAA AGTACAAGGC CATCCGGCTC
720
ATTTTGTCA TCATGGCGGT GTTTTTCATT TTCTGGACAC CCTACAATGT GGCTATCCTT
780
CTCTCTTCCT ATCAATCCAT CTTATTTGGA AATGACTGTG AGCGGAGCAA GCATCTGGAC
840
CTGGTCATGC TGGTGACAGA GGTGATCGCC TACTCCCACT GCTGCATGAA CCCGGTGATC
900
TACGCCTTTG TTGGAGAGAG GTTCCGGAAG TACCTGCGCC ACTTCTTCCA CAGGCACTTG
960
CTCATGCACC TGGGCAGATA CATCCCATTC CTTCCTAGTG AGAAGCTGGA AAGAACCAGC
1020
TCTGTCTCTC CATCCACAGC AGAGCCGGAA CTCTCTATTG TGTTT
1065

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3586 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```

GGATCCCTAC CTTCCCCATC AGAGCTAGGG GGCATGGAGC GCTCTCTGCT AAGATGGGGA
60
CCCCCAAGGA ATGTCTCCCT GTGGGGCACT TCCTTACCAG ATGGGATGGC CAGTGCGGTT
120
AAGTTGGTGG TCAGGCAGAA AAAAAAGATC TAGTTTGTAC TCTTGAGAGT TCCTCGGTTT
180
GTTTCATGGCA TGGGCAGGGA GTCAAGGAGC AGCAGCCTTG CCTCAGTGCC TACCAGTGCA
240
GGAAAAGGTG CATAGCCTGG GCCAGGGCCA GGGCCCTGGT GGAGGCGTAG TGGTAACAGA
300
GAGGGCTCTC CATTCCAGCC CAAGGAAGAC TAAGAATGAA TACCTCATGA GTATATTAGC
360
TACAAACCAC CACAGCAGGT TCCAGAAAAA GGCTCAGCGT TGAACCAGG TCACCCCCAC
420
TCAGCAGACA CCAGTCATAT AAATCAAGGA CCAACAGGAG ACAGGAACAC CCCCTTCCCA
480
CTCTGCCCCA TGTCTCAAGT TGTAGTGGCC CTTCTCTCCAG ATCTCTGCCA CCATCTTAGA
540
AAGGAACACT GAAAGAAGAA ACTGAAATTA TAAGCTGACA GCATAAAGAG GATGAGTAAA
600
ACCTAAAATC ATTGTTTACA TGAATGAATC AAGAGAAGTT TAAACCACTT TGGACTAAAA
660
TGTGTGAATC CTTTTTCCTG CTATCCAGCA GATGAGAAGC TGGTAACAGA GACCACAATA
720
GTTTGGAGAC TAAAGAATCA TTGCACATTT CACTGCTGAG TTGTATTGTG AGTAATTTTA
780
GTTGACCTCA CTTTGTAAT CTTGCACACG GGGCAATCCA ATATCTGCAC AAGAGATATG
840
TTAACCAGTG GTAAATGCTG CATGAGGAGA TTGGGTGATT TTTACTTTTCG TTTTGTGCT
900
CTTCTTTCTT ATTGTTCTTA CTTATTTACG ATTACCCTAT CGTTTTCCCA AAATGTAAAA
960
GGCCATTTTG AAAGCCTAAT TCAAACCTCT TCACTATTTT GTATCTAAGT ATTCACCTTG
1020
ATTGAGACTG GGTAGACAGG TGAAAACCAT ATCAGGTTTT TAATTTTTTA ATTTTAAAT
1080
ATTTATTTAT TTATTTATTT TTTGAGATGG AGTCTGGCTG TCGCCCAGGC TGGAGTGCAG
1140
CGGCGTGATC ACAGTTCAC TGCAGCCTCAA CCTTCTAGGC TCAAGGGATT CTCCCACCTC
1200
AGCCCCCAA GTAGTTGGGA CCACACGTAT GCGCCACCAT GCCTGGCTAA TTTCTTATTT
1260
TTTTGTAGAG ATAGGATCTC ACTATATTGT CCAGGCTGGT CTTGAATTCC TGGGCTCAGG
1320

```

TGAGCCTCCC ACCTGGGCCT CCCAAAGTAC TGGGATTACA GGCATGAGCC AAGGTCCCCT
1380
GCCCATATGA GATTTTCTGT CTCTGATCCC ATGCAGCTAG TAATCAAGGA CTTGGCTGCT
1440
GACTCTGGAG GACCTGCATG CTTTCTTGAG CTGTGAACTT CAGTGCTAAA AGCTCATAGG
1500
CAGCCCTGAA ACCCAAACCA AAAGGTTCCTA TGGTTTATCA TCCTGATCAT GTTGATTTTA
1560
TAGAAATAAC ACATGAATTA AAGACACTAC CCTCAAACCTG AGCAAACTT AAGTAATTTT
1620
TTTAAAGTTT GACCTGTTTT TAAATCACTC TTGGAGAAAA AGGAAAATAA ATACAAATAA
1680
TTAACGGTGA ATACAGGCTA CTATACCTTT GTTCTCCAGA ATTAGCAGTT CTGTTCTTTT
1740
CTTGCTTTAG ATGCTGAAGT GCAGAAGGAC ACTCTGTGAT TGTACGTGTG TAACTGACAA
1800
AATGTGTATT TTTTTTCTCA GCTGCTATGG ATTGGATTAT GCTATTATGA ATAAGAATGC
1860
TGATGGGAGC ACACACAAAC CATTTGTTCC TCAGTCCATT TTCCTCCTCA AAAGCCTGGA
1920
ATGTGCCATT GATCAGTGGG AGATGTACCT GGACAGACCC ATGAAAAGAG ATCAACAAGT
1980
TCCACCCAAG GGACCCTATT TTCCTAATT TCATTTGAAA TGGCTTCTAA TTGTCCTTCT
2040
TTCATTCCTG CTCCTACCA GTTTTACAGC TTTTCTGGT TTCAAATGTG AACTCACATA
2100
CACTCTCATT TTCCTCATC ACAACCCCAA GTGACCCAAT GGTCTCACT TTCGATATAA
2160
GTAAAGGAGG CTCTGCATTA AGGGCTTGTC CAAGGCACGC AGCTGAGAGG CGCTAGGACT
2220
GGCTCCATTT CCATCTCTAT TCTCACTGAC TTTGACTACC CAGAACCCCA ACATGTGGGG
2280
CCTCAGTATT CGATCAATTA TTCTATTAAG AAGCAAAAAC AATTCCCCGC ATTGGCCCCA
2340
GTTATTAAGC ATTTCTCAGA TTTACCTTGA GAAATGCCCA TCGGCCTGTA TATTCACATC
2400
TTCACCCTTG TCCCTTCCTC CTAGAAAGGA GAAAGTCAGT TGGATGCCCT CTGAGGAACT
2460
AGTGCATGGC TTAACGTGCC TTCCATGACT CCTGCCTTAT CTGTTTTCTA TTTTCCTCCT
2520
TTTCCACCGA AGTCTATAAT CTCAAGAAAA GCAGGCACTG GCCTTAGGGC TCCTGGCCTA
2580
AGAAATATCA AGTCCAGTGA GAAATCCCAT TGA CTGAGCCC CTCCTGCTTA CCCCTTTGTG
2640
ATGGAGAAGC TCCCAGGGGT TTGCTTTTTG CATGTTACCA GGCCTAACTC AGCATCACCA
2700
GGGGCAAGAA AAGGAAAGTA ACCTAAACTA ATGCTGCTTA TAATTGTAAT TATTGTAATA
2760
GTTAATTACT GTGATTGTAC ATGTGTAACA GACAAAATGT GTATTTTTTT CACAGCTGCT
2820
GTGGATTGGA TTATGCCATT TGGAATAAGA ATGCTGTAA GAGCACACAA GCCAGGTTCC
2880
TCAAGTCCGT AGCAAATTTT TCAAAAGTTA AATTTAAAAA TCACTACATT TGAATCTAGT
2940
GACAGGAGAA ATGGACATGG ATAGAGACTA AAGATCTAGC CCAAATTTTA TATTTACTTG
3000

TTAGAGGATT TTGAACAAAT TACTAAATTT CTTCAAGGTT CAATTTCCCC ATTA ACTATA
3060
ATGAATGTCT CATCATTATG GGGCCCTGGA GAAGCATAAT TACTTGTAAT TGTAATAATC
3120
ATTGTTATTA TTATTATACA TATTTTGCTT TTAAATGGAT AAGGATTTT AAGGTATATG
3180
TAAACTGTAA AACATAAAAT GCAAAATGCC GTAAGAGACA GTAGTAATAA TAATGATTAT
3240
TATATTGTTA TCATTATCTA GCCTGTTTTT TCCTGTTGTG TATTTCTTCC TTAAATGCT
3300
TACAGAAATC TGTATCCCCA TTCTTCACCA CCACCCACACA ACATTTCTGC TTCTTTTCCC
3360
ATGCCGGTCA TGCTAACTTT GAAAGCTTCA GCTCTTTCCT TCCTCAATCC TTCTCCTGGC
3420
ACCTCTGATA TGCCTTTTGA AATTCATGTT AAAGAATCCC TAGGCTGCTA TCACATGTGG
3480
CATCTTTGTT GAGTACATGA ATAAATCAAC TGGTGTGTTT TACGAAGGAT GATTATGCTT
3540
CATTGTGGGA TTGTATTTT CTTCTTCTAT CACAGGGAGA AGTGAA
3586

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 448 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TAGGTCAGAT GCAGAAAATT GCCTAAAGAG GAAGGACCAA GGAGATGAAG CAAACACATT
60
AAGCCTTCCA CACTCACCTC TAAACAGTC CTTCAAACCT CCAGTGCAAC ACTGAAGCTC
120
TTGAAGACAC TGAAATATAC ACACAGCAGT AGCAGTAGAT GCATGTACCC TAAGGTCATT
180
ACCACAGGCC AGGGGCTGGG CAGCGTACTC ATCATCAACC CTAAAAGCA GAGCTTTGCT
240
TCTCTCTCTA AAATGAGTTA CCTACATTTT AATGCACCTG AATGTTAGAT AGTTACTATA
300
TGCCGCTACA AAAAGGTAAA ACTTTTATA TTTTATACAT TAACTTCAGC CAGCTATTGA
360
TATAAATAAA ACATTTTCAC ACAATACAAT AAGTTAACTA TTTTATTTTC TAATGTGCCT
420
AGTTCTTTCC CTGCTTAATG AAAAGCTT
448